

Art Unit: 1652

APPENDIX A

AC P35749; O00396; O94944; P78422;

Query Match 98.5%; Score 3564.5; DB 1; Length 1972;
Best Local Similarity 99.0%; Pred. No. 1.2e-211;
Matches 692; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

Qy 1 MAQKGQLSDDEKFLFVDKNFINSVPAQADWAAKRLVWVPSEKQGFEEASIKEEKGDEVVV 60
|||
Db 1 MAQKGQLSDDEKFLFVDKNFINSVPAQADWAAKRLVWVPSEKQGFEEASIKEEKGDEVVV 60

Qy 61 ELVENGKKVTVGKDDIQMNPPKFSKVEDMAELTCLNEASVLHNLRLRERYFSGLIYTYSGL 120
|||
Db 61 ELVENGKKVTVGKDDIQMNPPKFSKVEDMAELTCLNEASVLHNLRLRERYFSGLIYTYSGL 120

Qy 121 FCVVVNPYKHLPIYSEKIVDMYKGKKRHEMPPHIYAIADTAYRSMQLQDREDQSILCTGES 180
|||
Db 121 FCVVVNPYKHLPIYSEKIVDMYKGKKRHEMPPHIYAIADTAYRSMQLQDREDQSILCTGES 180

Qy 181 GAGKTENTKKVIQYLAVVASSHKGKDTSTITQGPSFAYGELEKQLLQANPILEAFGNAKT 240
|||
Db 181 GAGKTENTKKVIQYLAVVASSHKGKDTSTIT-----GELEKQLLQANPILEAFGNAKT 233

Qy 241 VKNDNSSRFGKFIRINFVDTGYIVGANIETYLLEKSRAIRQARDERTFHIFYMIAGAKE 300
|||
Db 234 VKNDNSSRFGKFIRINFVDTGYIVGANIETYLLEKSRAIRQARDERTFHIFYMIAGAKE 293

Qy 301 KMRSDDLLEGFNNYTFLSNGFVPIPAAQDDEMFQETVEAMAIMGFSEEEQLSILKVVSSV 360
|||
Db 294 KMRSDDLLEGFNNYTFLSNGFVPIPAAQDDEMFQETVEAMAIMGFSEEEQLSILKVVSSV 353

Qy 361 LQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIKVGRDVVQKAQT 420
|||
Db 354 LQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIKVGRDVVQKAQT 413

Qy 421 KEQADFAVEALAKATYERLFRWILTRVNKALDKTHRQASFLGILDIAGFIFEVNSFEQ 480
|||
Db 414 KEQADFAVEALAKATYERLFRWILTRVNKALDKTHRQASFLGILDIAGFIFEVNSFEQ 473

Qy 481 LCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPGVLA 540
|||
Db 474 LCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPGVLA 533

Qy 541 LLDEECWFPAKTDKSFVEKLCTEQGSHPKFKPKQLKDKTEFSIIHYAGKVDYNASAWLT 600
|||
Db 534 LLDEECWFPAKTDKSFVEKLCTEQGSHPKFKPKQLKDKTEFSIIHYAGKVDYNASAWLT 593

Qy 601 KNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTV 660
|||
Db 594 KNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTV 653

Qy 661 GQLYKEQLGKLMTTLRNTTPNFVRCIIPNHEKRSGKLDA 699
|||
Db 654 GQLYKEQLGKLMTTLRNTTPNFVRCIIPNHEKRSGKLDA 692

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APPENDIX B

AB020673
FEATURES

source	1. .6846 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="hk00546s1" /tissue_type="brain" /clone_lib="pBluescriptII SK plus"
gene	1. .6846 /gene="KIAA0866"
CDS	<40. .5994 /gene="KIAA0866" /note="This sequence was replaced that of hk06733 cDNA as a representative cDNA sequence for KIAA0866." /codon_start=1 /product="KIAA0866 protein" /protein_id="BAA74889.2" /db_xref="GI:27529744" /translation="SPQLEIWDQQGTMAQKQGLSDDEKFLFVDKNFINSPVAQADWAA KRLVWVPSEKQGFEEAASIKKEKGDEVVVELVENGKKVTVGKDDIQKMNPPKFSKVEDM AELTCLNEASVLHNLRRERYFSGLIYTYSGLFCVVVNPYKHLPIYSEKIVDMYKGGKRH EMPPHIYAIADTAYRSMQLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKK DTSITGELEKQLLQANPILEAFGNAKTVMKNDNSSRFGKFIRINFDVVTGYIVGANIETY LLEKSRAIRQARDERTFHFYMIAGAKEKMRSDLLLEGFNNTFLSNGFVPIPAQD DEMFQETVEAMAIMGFSEEEQLSILKVVSSVLQLGNIVFKKERNTDQASMPDNTAAQK VCHLMGINVTDFTSRILTPIKVGDRVQKAQTKQADFAVEALAKATYERLFRWILT RVNKALDKTHRQASFLGILDIAQFEIFEVNSFEQLCINYNTEKQLQFLNHTMFILEQ EEYQREGIEWNFIDFGDLQPCIELIERPNNPPGVLALLDEECWFPKATDKSFVEKLC TEQGSHPKFKQPKQLKDKTEFSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLNASSD KFVADLWKDVRIVGLDQMAKMTESLPSASKTKKGMFRTVGQLYKEQLGKLMTTLRN TTPNFVRCIIPNHEKRSGLDAFLVLVLEQLRCNGVLEGIRICRQGFPPNRIVFQEFQRQY EILAANAIPKGFMDGKQACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEEEERDLKI TDVIMAFQAMCRGYLARKAFARQQQLTAMKVIQRNCAAYLKLRNWQWWRLFTKVKPL LQVTRQEEEMQAKEDLQKTKERQKKAENELKELEQKHSQLEEKNNLLQEQQLAETEL YAEAEEMRVRLAAKKQELEEILHEMEARLEEEEDRGQQLQAERKKMAQQMLDLEEQL EEEAARQKLQLEKVTAIAKIKKLEDEILVMDDQNNKLSKERKLEERISDLTTNLAAE EEKAKNLTCLKNKHESMISELEVRLKKEEKSQRQLEKLRKLEGDASDFHEQIADLQA QIAELKMLAKKEEELQAALARLDDEIAQKNNAKKIRELEGGHISDLQEDLDSERAAR NKAQKQKRDLEGELEALKTELEDTLSTATQQLRAKREQEVTVLKKALDEETRSHEA QVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQTLKENADLAGELRVLGQAQEV EHKKKKLEAQVQELQSKCSDGERARAEELNDKVHKLQNEVESVTGMLNEAEGKAIKLAK DVASLSSQLQDTQELLQEBTRQKLNVTSTKLRLQLEEBERNSLQDQLDEEMEAKQNLERHI STLNIQLSDSKKKLQDFASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLETKNR LQQELDDLVDLDNRQLVSNLEKKQKQKFDQLLAEKNISSKYADERDRAEAEAREKE TKALSLARALEEAELEELERTNKMLKAEMEDLVSSKDDVGKNVHELEKSKRALETQ MEEMKTQLEEELEDELQATEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQL HEYETELEDERKQRAAAAAKKKLEGLDKDELQADSAIKGEEAIKQLRKLQAQMKD FQRELEDARASRDEIFATAKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKEELA EELASSLSGRNALQDEKRRLEARIAQLEEELEEEQGNMEAMSDRVKATQQAQELSNE LATERSTAQKNESARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEEQV EQEAREKQAATKSLKQDKKLKEILLQVEDERKMAEQYKEQAQKGNARVKQLKRQLEE AEEESQRINANRRKLQRELDEATESNEAMGREVNALKSKLRRGNETSFVPSRRSGGRR VIENADGSEETDTRDADFNQTKASE"

ORIGIN

Alignment Scores:

Pred. No.:	3.95e-263	Length:	6846
Score:	3564.50	Matches:	692
Percent Similarity:	99.00%	Conservative:	0
Best Local Similarity:	99.00%	Mismatches:	0
Query Match:	98.55%	Indels:	7
DB:	9	Gaps:	1

US-09-927-597-6 (1-699) x AB020673 (1-6846)

Qy	1	MetAlaGlnLysGlyGlnLeuSerAspAspGluLysPheLeuPheValAspLysAsnPhe	20
Db	76	ATGGCGCAGAAGGGCCAACTCAGTGACGATGAGAAGTTCCTCTTGTGTGGACAAAACTTC	135
Qy	21	IleAsnSerProValAlaGlnAlaAspTrpAlaAlaLysArgLeuValTrpValProSer	40
Db	136	ATCAACAGCCCACTGGCCCAAGGCTGACTGGGCGCCCAAGAGACTCGTCTGGGTCCCTCG	195
Qy	41	GluLysGlnGlyPheGluAlaAlaSerIleLysGluGluLysGlyAspGluValValVal	60
Db	196	GAGAAGCAGGGCTTCGAGGCAGCCAGCATTAAGGAGGAGAAGGGGATGAGGTGGTTGTG	255
Qy	61	GluLeuValGluAsnGlyLysLysValThrValGlyLysAspAspIleGlnLysMetAsn	80
Db	256	GAGCTGGTGAGAATGGCAAGAAGGTACGGTTGGGAAAGATGACATCCAGAAGATGAAC	315
Qy	81	ProProLysPheSerLysValGluAspMetAlaGluLeuThrCysLeuAsnGluAlaSer	100
Db	316	CCACCCAAGTTCTCCAAGGTGGAGGACATGGCGGAGCTGACGTGCCTCAACGAAGCCTCC	375
Qy	101	ValLeuHisAsnLeuArgGluArgTyrPheSerGlyLeuIleTyrThrTyrSerGlyLeu	120
Db	376	GTGTACACAACCTTGAGGGAGCGGTACTTCTCAGGGCTAATATATACGTACTCTGGCCTC	435
Qy	121	PheCysValValValAsnProTyrLysHisLeuProIleTyrSerGluLysIleValAsp	140
Db	436	TTCTGCGTGGTGGTCAACCCCTATAAACACCTGCCCATCTACTCGGAGAAGATCGTCGAC	495
Qy	141	MetTyrLysGlyLysLysArgHisGluMetProProHisIleTyrAlaIleAlaAspThr	160
Db	496	ATGTACAAGGGCAAGAAGAGGCACGAGATGCCGCCTCACATCTACGCCATCGCAGACACG	555
Qy	161	AlaTyrArgSerMetLeuGlnAspArgGluAspGlnSerIleLeuCysThrGlyGluSer	180
Db	556	GCCTACCGGAGCATGCTTCAAGATCGGGAGGACCAGTCCATTCTATGCACAGGCGAGTCT	615
Qy	181	GlyAlaGlyLysThrGluAsnThrLysLysValIleGlnTyrLeuAlaValValAlaSer	200
Db	616	GGAGCCGGGAAAACCGAAAACACCAAGAAGGTCATTTCAGTACCTGGCCGTGGTGGCCTCC	675
Qy	201	SerHisLysGlyLysLysAspThrSerIleThrGlnGlyProSerPheAlaTyrGlyGlu	220
Db	676	TCCCACAAGGGCAAGAAAGACACAAGTATCAGC-----GGAGAG	714
Qy	221	LeuGluLysGlnLeuLeuGlnAlaAsnProIleLeuGluAlaPheGlyAsnAlaLysThr	240
Db	715	CTGGAAGCAGCTTCTACAAGCAAACCCGATTCTGGAGGCTTTCGGCAACGCCAAAACA	774
Qy	241	ValLysAsnAspAsnSerSerArgPheGlyLysPheIleArgIleAsnPheAspValThr	260
Db	775	GTGAAGAACGACAACTCCTCAGATTGCGCAAATTCATCCGCATCAACTTCGACGTCACG	834
Qy	261	GlyTyrIleValGlyAlaAsnIleGluThrTyrLeuLeuGluLysSerArgAlaIleArg	280
Db	835	GGTTACATCGTGGGAGCCAACATTGAGACCTATCTGCTAGAAAAATCACGGGCAATTGCG	894
Qy	281	GlnAlaArgAspGluArgThrPheHisIlePheTyrTyrMetIleAlaGlyAlaLysGlu	300
Db	895	CAAGCCAGAGACGAGAGGACATTCACATCTTTTACTACATGATTGCTGGAGCCAAGGAG	954
Qy	301	LysMetArgSerAspLeuLeuLeuGluGlyPheAsnAsnTyrThrPheLeuSerAsnGly	320
Db	955	AAGATGAGAAGTGACTTGCTTTTGGAGGGCTTCAACAACACCTTCTCTCCAATGGC	1014
Qy	321	PheValProIleProAlaAlaGlnAspAspGluMetPheGlnGluThrValGluAlaMet	340
Db	1015	TTTGTGCCCATCCAGCAGCCAGGATGATGAGATGTTCCAGGAAACCGTGGAGGCCATG	1074
Qy	341	AlaIleMetGlyPheSerGluGluGluGlnLeuSerIleLeuLysValValSerSerVal	360

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|||||
Db 1075 GCAATCATGGGTTTCAGCGAGGAGGAGCAGCTATCCATATTGAAGGTGGTATCATCGGTC 1134
Qy 361 LeuGlnLeuGlyAsnIleValPheLysLysGluArgAsnThrAspGlnAlaSerMetPro 380
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Db 1135 CTGCAGCTTGGAATATCGTCTTCAAGAAGGAAAGAAACACAGACCAGGCGTCCATGCCA 1194
Qy 381 AspAsnThrAlaAlaGlnLysValCysHisLeuMetGlyIleAsnValThrAspPheThr 400
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Db 1195 GATAACACAGCTGCTCAGAAAGTTTGCCACCTCATGGGAATTAATGTGACAGATTTCACC 1254
Qy 401 ArgSerIleLeuThrProArgIleLysValGlyArgAspValValGlnLysAlaGlnThr 420
|||||
Db 1255 AGATCCATCCTCACTCCTCGTATCAAGGTGGGCGAGATGTGGTACAGAAAGCTCAGACA 1314
Qy 421 LysGluGlnAlaAspPheAlaValGluAlaLeuAlaLysAlaThrTyrGluArgLeuPhe 440
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Db 1315 AAAGAACAGGCTGACTTTGCTGTAGAGGCTTTGGCCAAGGCAACATATGAGCGCCTTTTC 1374
Qy 441 ArgTrpIleLeuThrArgValAsnLysAlaLeuAspLysThrHisArgGlnGlyAlaSer 460
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Db 1375 CGCTGGATACTACCCGCGTGAACAAAGCCCTGGACAAGACCCATCGGCAAGGGGCTTCC 1434
Qy 461 PheLeuGlyIleLeuAspIleAlaGlyPheGluIlePheGluValAsnSerPheGluGln 480
|||||
Db 1435 TTCTGGGGATCCTGGATATAGCTGGATTTGAGATCTTTGAGGTGAACCTTCGAGCAG 1494
Qy 481 LeuCysIleAsnTyrThrAsnGluLysLeuGlnGlnLeuPheAsnHisThrMetPheIle 500
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Db 1495 CTGTGCATCAACTACCAACGAGAAGCTGCAGCAGCTCTTCAACCACCATGTTTCATC 1554
Qy 501 LeuGluGlnGluGluTyrGlnArgGluGlyIleGluTrpAsnPheIleAspPheGlyLeu 520
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Db 1555 CTGGAGCAGGAGGAGTACCAGCGCAGGGCATCGAGTGAACCTTCATCGACTTTGGGCTG 1614
Qy 521 AspLeuGlnProCysIleGluLeuIleGluArgProAsnAsnProProGlyValLeuAla 540
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Db 1615 GACCTACAGCCCTGCATCGAGCTCATCGAGCGACCGAACAACCTCCAGGTGTGCTGGCC 1674
Qy 541 LeuLeuAspGluGluCysTrpPheProLysAlaThrAspLysSerPheValGluLysLeu 560
|||||
Db 1675 CTGCTGGACGAGGAATGCTGTTCCCAAAGCCACGACAAGTCTTTCGTGGAGAAGCTG 1734
Qy 561 CysThrGluGlnGlySerHisProLysPheGlnLysProLysGlnLeuLysAspLysThr 580
|||||
Db 1735 TGCACGAGCAGGGCAGCCACCCCAAGTTCCAGAAGCCAAGCAGCTCAAGGACAAGACT 1794
Qy 581 GluPheSerIleIleHisTyrAlaGlyLysValAspTyrAsnAlaSerAlaTrpLeuThr 600
|||||
Db 1795 GAGTTCTCCATCATCCATTATGCTGGGAAGGTGGACTATAATGCGAGTGCCTGGCTGACC 1854
Qy 601 LysAsnMetAspProLeuAsnAspAsnValThrSerLeuLeuAsnAlaSerSerAspLys 620
|||||
Db 1855 AAGAATATGGACCCGCTGAATGACAACGTGACTTCCCTGCTCAATGCCTCCTCCGACAAG 1914
Qy 621 PheValAlaAspLeuTrpLysAspValAspArgIleValGlyLeuAspGlnMetAlaLys 640
|||||
Db 1915 TTTGTGGCCGACCTGTGGAAGGACGTGGACCGCATCGTGGGCTTGACACAGATGGCCAAG 1974
Qy 641 MetThrGluSerSerLeuProSerAlaSerLysThrLysLysGlyMetPheArgThrVal 660
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Db 1975 ATGACGGAGAGCTCGCTGCCAGCGCCTCCAAGACCAAGAAGGGCATGTTCGCACAGTG 2034
Qy 661 GlyGlnLeuTyrLysGluGlnLeuGlyLysLeuMetThrThrLeuArgAsnThrThrPro 680
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Db 2035 GGGCAGCTGTACAAGGAGCAGCTGGGCAAGCTGATGACCACGCTACGCAACACCACGCCC 2094
Qy 681 AsnPheValArgCysIleIleProAsnHisGluLysArgSerGlyLysLeuAspAla 699
|||||

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Db 2095 AACTTCGTGCGCTGCATCATCCCCAACCACGAGAAGAGGTCCGGCAAGCTGGATGCG 2151